

Compd #	MOLSTRUCTURE
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FIGURE 1A

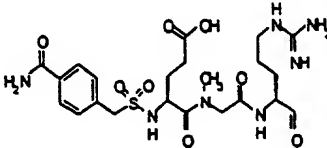
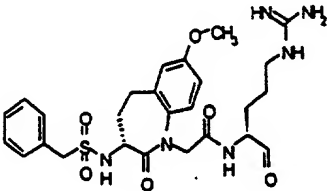
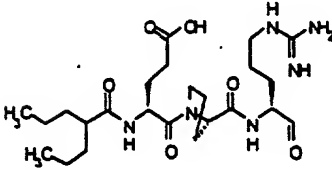
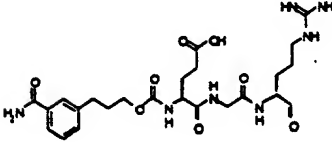
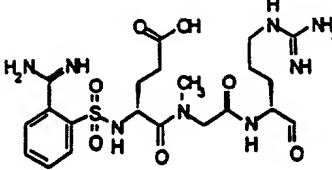
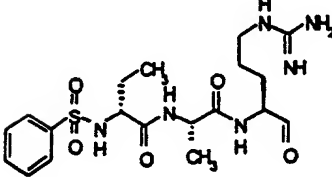
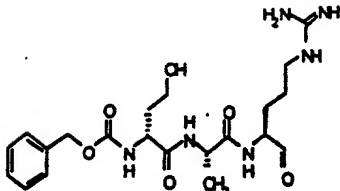
Compd #	MOLSTRUCTURE
8	
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FIGURE 1B

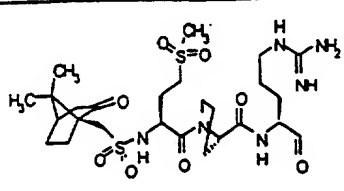
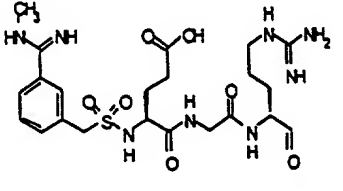
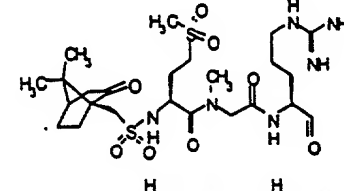
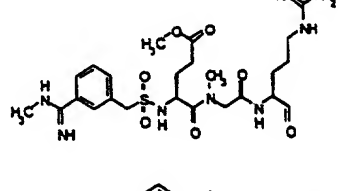
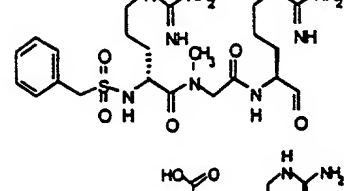
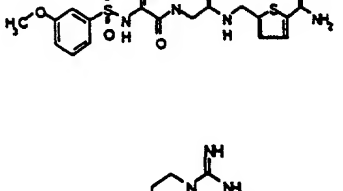
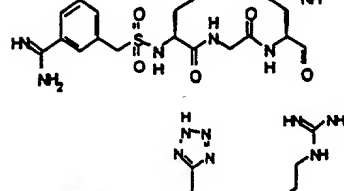
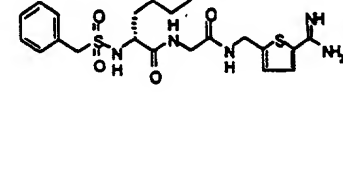
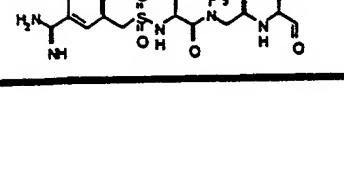
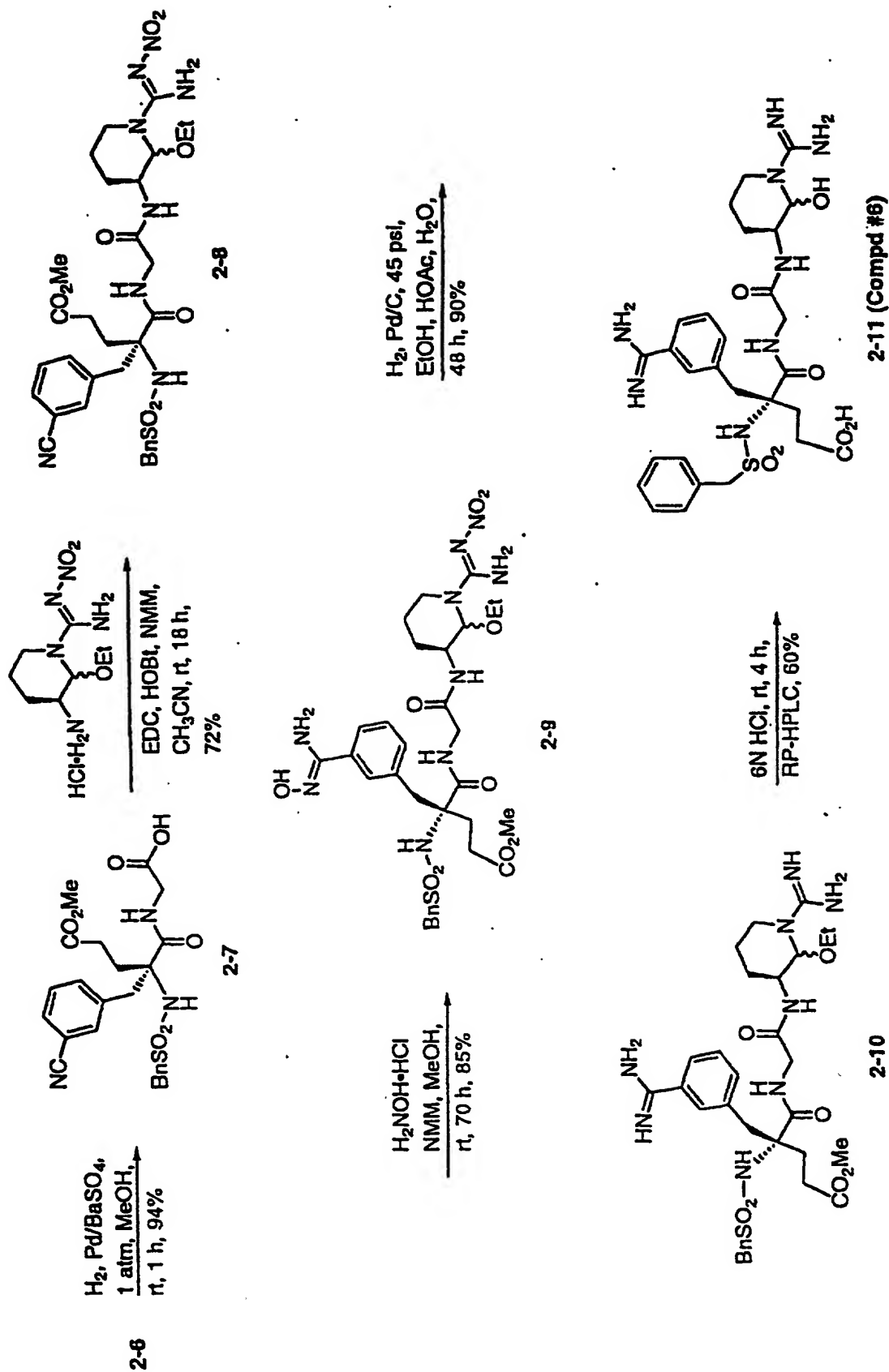
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
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FIGURE 1C





10            20            30            40            50            60  
 GTTGTGTTTTGACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT  
 CAACAACCCCGTGCCTACGCCTACTCCCGCTCACCGGGACCGTCCATTTCGGACGTACGA  
 V V G G T D A D E G E W P W Q V S L H A>  
 70            80            90            100            110            120  
 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC  
 GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG  
 L G Q G H I C G A S L I S P N W L V S A>  
 130            140            150            160            170            180  
 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCACGCAGTGGACGGCC  
 CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCCTCACCTGCCGG  
 A H C Y I D D R G F R Y S D P T Q W T A>  
 190            200            210            220            230            240  
 TTCCTGGGCTTGACGACCAGAGCCAGCGCAGCGCCCTGGGGTGCAGGAGCGCAGGCTC  
 AAGGACCCGAACGTGCTGGTCTCGGTGCGGTGCGGGGACCCACGTCTCTCGCGTCCGAG  
 F L G L H D Q S Q R S A P G V Q E R R L>  
 250            260            270            280            290            300  
 AAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG  
 TTCGCGTAGTAGAGGTGGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC  
 K R I I S H P F F N D F T F D Y D I A L>  
 310            320            330            340            350            360  
 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGGGCCCCATCTGCCTGCCGGAC  
 GACCTCGACCTCTTTGGCCGTCTCATGTGAGGTACCACGCCGGGTAGACGGACGGCCTG  
 L E L E K P A E Y S S M V R P I C L P D>

FIGURE 3A

370            380            390            400            410            420  
 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGGACACACCCAG  
 CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC  
 A S H V F P A G K A I W V T G W G H T Q>  
  
 430            440            450            460            470            480  
 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC  
 ATACCTCCGTGACCGCGCGACTAGGACGTTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG  
 Y G G T G A L I L Q K G E I R V I N Q T>  
  
 490            500            510            520            530            540  
 ACCTGCGAGAACCTCCTGCCGCGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC  
 TGGACGCTCTTGGAGGACGGCGCTCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG  
 T C E N L L P Q Q I T P R M M C V G F L>  
  
 550            560            570            580            590            600  
 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG  
 TCGCCGCGCGACCTGAGGACGGTCCCACTAAGGCCCCCTGGGGACAGGTCCGACCTCCGC  
 S G G V D S C Q G D S G G P L S S V E A>  
  
 610            620            630            640            650            660  
 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC  
 CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG  
 D G R I F Q A G V V S W G D G C A Q R N>  
  
 670            680            690            700            710            720  
 AAGCCAGGCGTGACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG  
 TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTCTTGTGACCC  
 K P G V Y T R L P L F R D W I K E N T G>

FIGURE 3B

GTATAG

CATATC

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FIGURE 3C

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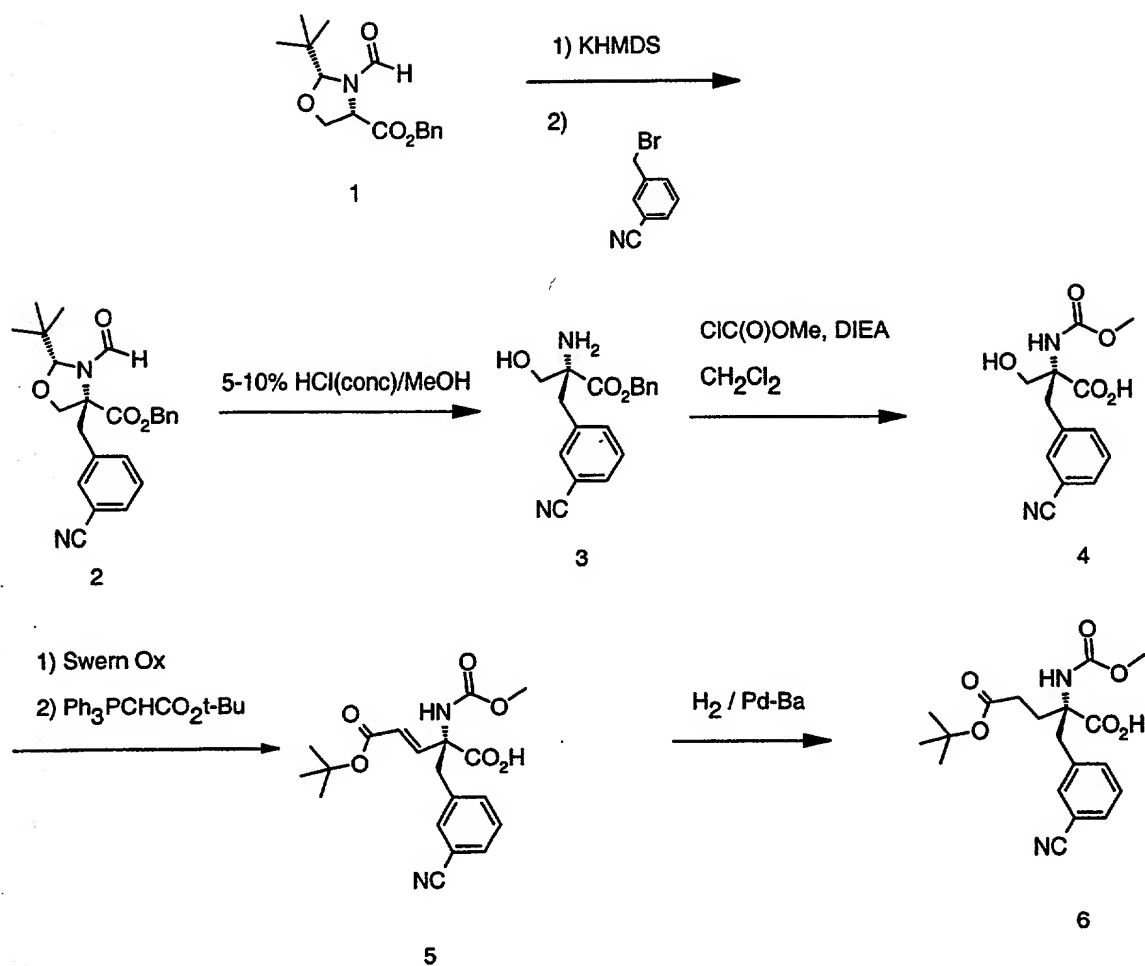


FIGURE 4A



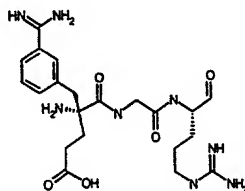
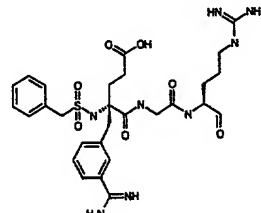
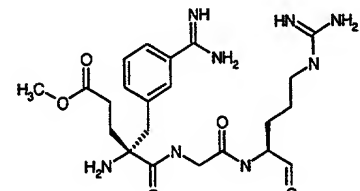
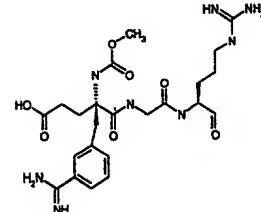
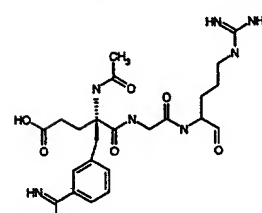
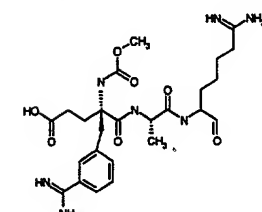
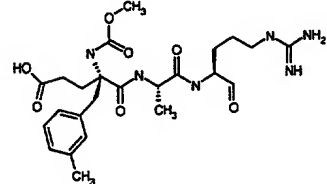
Compound	Structure
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FIGURE 5A

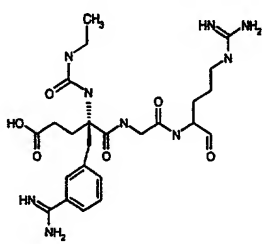
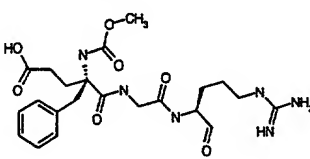
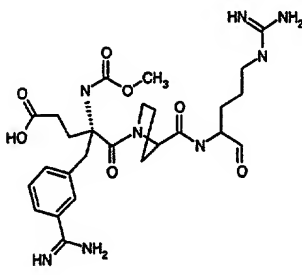
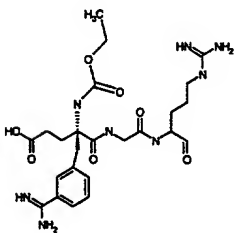
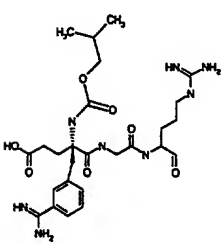
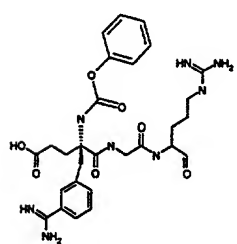
Compound	Structure
H	
I	
J	
K	
L	
M	

FIGURE 5B